

Applicant : Ikuo Matsui et al.
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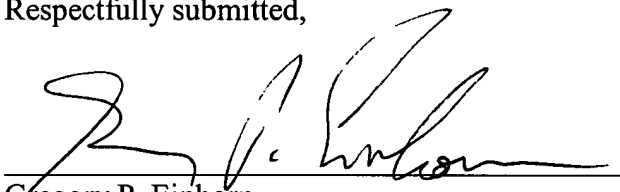
REMARKS

Applicant hereby submits that the enclosures fulfill the requirements under 37 C.F.R. §1.821-1.825 and that no new matter is added. Please insert the paper copy of the Sequence Listing on page 28, replacing the existing sequence listing on page 28. Attached is a marked-up version of the changes being made by the current amendment.

Please apply any other charges or credits to Deposit Account No. 06-1050.

Respectfully submitted,

Date: May 7, 2001



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Version with markings to show changes made

In the specification:

Paragraph beginning at page 5, line 24 has been amended as follows:

Figure 5 shows aligned amino acid sequences of five α -glycosidases from hyperthermophilic archaea. The abbreviations of the sources of the enzymes are: BGPh, α -glycosidase from *P. horikoshii* (SEQ ID NO: 5); BMPH, a α -mannosidase gene homolog from *P. horikoshii* (8,9)(SEQ ID NO: 6); BGPf, α -glucosidase from *P. furiosus* (17)(SEQ ID NO: 8); BMPf, α -mannosidase from *P. furiosus* (17)(SEQ ID NO: 7); S-gly, α -glycosidase from *Sulfolobus solfataricus* (18)(SEQ ID NO: 9); and the Consensus sequence (SEQ ID NO: 10). The conserved residues, identified automatically by the GeneWorks program, are shown in the open boxes. The reversed open triangles indicate the location of the nucleophile (E324) and the putative acid/base catalyst (E155 and H111) with R75 in the spatial proximity of the nucleophile of BGPh. The arrow shows the prominent deletion of more than 30 residues found in BGPh.